

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Timothy A.  
Rosen, Craig A.
- (ii) TITLE OF INVENTION: Endothelial Monocyte Activating  
Polypeptide III
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Avenue  
(C) CITY: Rockville,  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20850
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/972,301  
(B) FILING DATE: 18-NOV-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/483,534  
(B) FILING DATE: 07-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Marks, Michelle S.  
(B) REGISTRATION NUMBER: 41,971  
(C) REFERENCE/DOCKET NUMBER: PF206D1
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 301-309-8504  
(B) TELEFAX: 301-309-8439

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 636 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 94..597

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACCCCTGCC CTGAAAAAAC TGGCCAGCGC TGCCTACCCA GATCCCTCAA AGCAGAAGCC 60  
 AATGGCCAAA GGCCTGCCAA GAATTCAGAA CCA GAG GAG GTC ATC CCA TCC CGG 114  
 Glu Glu Val Ile Pro Ser Arg  
 1 5  
 CTG GAT ATC CGT GTG GGG AAA ATC ATC ACT GTG GAG AAG CAC CCA GAT 162  
 Leu Asp Ile Arg Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp  
 10 15 20  
 GCA GAC AGC CTG TAT GTA GAG AAG ATT GAC GTG GGG GAA GCT GAA CCA 210  
 Ala Asp Ser Leu Tyr Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro  
 25 30 35  
 CGG ACT GTG GTG AGC GGC CTG GTA CAG TTC GTG CCC AAG GAG GAA CTG 258  
 Arg Thr Val Val Ser Gly Leu Val Gln Phe Val Pro Lys Glu Glu Leu  
 40 45 50 55  
 CAG GAC AGG CTG GTA GTG GTG CTG TGC AAC CTG AAA CCC CAG AAG ATG 306  
 Gln Asp Arg Leu Val Val Val Leu Cys Asn Leu Lys Pro Gln Lys Met  
 60 65 70  
 AGA GGA GTC GAG TCC CAA GGC ATG CTT CTG TGT GCT TCT ATA GAA GGG 354  
 Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly  
 75 80 85  
 ATA AAC CGC CAG GTT GAA CCT CTG GAC CCT CCG GCA GGC TCT GCT CCT 402  
 Ile Asn Arg Gln Val Glu Pro Leu Asp Pro Pro Ala Gly Ser Ala Pro  
 90 95 100  
 GGT GAG CAC GTG TTT GTG AAG GGC TAT GAA AAG GGC CAA CCA GAT GAG 450  
 Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu  
 105 110 115  
 GAG CTC AAG CCC AAG AAG AAA GTC TTC GAG AAG TTG CAG GCT GAC TTC 498  
 Glu Leu Lys Pro Lys Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe  
 120 125 130 135  
 AAA ATT TCT GAG GAG TGC ATC GCA CAG TGG AAG CAA ACC AAC TTC ATG 546  
 Lys Ile Ser Glu Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met  
 140 145 150  
 ACC AAG CTG GGC TCC ATT TCC TGT AAA TCG CTG AAA GGG GGG AAC ATT 594  
 Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile  
 155 160 165  
 AGC TAGCCAGCCC AGCATCTTCC CCCCTTCTTC CACCACTGA 636  
 Ser

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile
 1           5           10           15
Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile
          20           25           30
Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu Val Gln
          35           40           45
Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val Leu Cys
          50           55           60
Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly Met Leu
          65           70           75           80
Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro Leu Asp
          85           90           95
Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys Gly Tyr
          100          105          110
Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Lys Val Phe
          115          120          125
Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln
          130          135          140
Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys
          145          150          155          160
Ser Leu Lys Gly Gly Asn Ile Ser
          165

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGGATCC GAGGAGGTCA TCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 28 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCAAGCTT CTAGATAATG TTCCCCC

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC GAGGAGGTCA TCCCATCC

28

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCGGATCC CTAGATAATG TTCCCCC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 183 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser Ala  
 1 5 10 15  
 Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly Cys  
 20 25 30  
 Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu  
 35 40 45  
 Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly Leu  
 50 55 60  
 Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile Leu  
 65 70 75 80  
 Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Lys Ser Gln Ala  
 85 90 95  
 Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala Pro  
 100 105 110  
 Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe Pro  
 115 120 125  
 Gly Glu Pro Asp Lys Glu Lys Asn Pro Lys Lys Lys Ile Trp Glu Gln  
 130 135 140  
 Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr Lys  
 145 150 155 160  
 Glu Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln Thr  
 165 170 175  
 Met Ser Asn Ser Gly Ile Lys  
 180

Sub  
 82  
 cont